



CHIR0157 (updated 06-06-06).ST25.txt  
SEQUENCE LISTING

<110> Covacci, Antonello  
Bugnoli, Massimo  
Telford, John  
Macchia, Giovanni  
Rappuoli, Rino

<120> Helicobacter Pylori CAI Antigen Polynucleotides

<130> CHIR0157

<140> 09/360,685

<141> 1999-07-26

<150> 08/471,491

<151> 1995-06-06

<150> 08/256,848

<151> 1994-10-21

<160> 30

<170> PatentIn version 3.3

<210> 1

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<223> primer oligonucleotide

<400> 1

gcaagcttat cgatgtcgac tcgagct

27

<210> 2

<211> 3960

<212> DNA

<213> Helicobacter pylori

<400> 2

aaaaagaaag gaagaaaatg gaaatacaac aaacacaccg caaaatcaat cgccctctgg 60

tttctctcgc tttagtagga gcattagtca gcatcacacc gcaacaaagt catgccgcct 120

ttttcacaac cgtgatcatt ccagccattg ttgggggtat cgctacaggc accgctgtag 180

gaacggtctc agggcttctt agctgggggc tcaaacaagc cgaagaagcc aataaaaccc 240

cagataaacc cgataaagtt tggcgcattc aagcaggaaa aggctttaat gaattcccta 300

acaaggaata cgacttatac agatcccttt tatccagtaa gattgatgga ggttgggatt 360

gggggaatgc cgctaggcat tattgggtca aaggcgggca acagaataag cttgaagtgg 420

atatgaaaga cgctgtaggg acttatacct tatcagggct tagaaacttt actggtgggg 480

atttagatgt caatatgcaa aaagccactt tacgcttggg ccaattcaat ggcaattctt 540

ttacaagcta taaggatagt gctgatcgca ccacgagagt ggatttcaac gctaaaaata 600

tctcaattga taattttgta gaaatcaaca atcgtgtggg ttctggagcc gggaggaaag 660

ccagctctac ggttttgact ttgcaagctt cagaagggat cactagcgat aaaaacgctg 720

aaatttctct ttatgatggt gccacgctca atttggttc aagcagcggt aaattaatgg 780

## CHIR0157 (updated 06-06-06).ST25.txt

gtaatgtgtg	gatggggccgt	ttgcaatac	g	tggaagcgta	tttggcccct	tcatacagca	840
cgataaacac	ttcaaaagta	acaggggaag	t	gaatttttaa	ccacctcact	gttggcgata	900
aaaacgccgc	tcaagcgggc	attatcgcta	a	taaaaaagac	taatattggc	acactggatt	960
tgtggcaaa	cgccgggtta	aacattatcg	c	tcctccaga	aggtggctat	aaggataaac	1020
ccaataatac	cccttctcaa	agtgggtgcta	a	aaacgacaa	aatgaaagc	gctaaaaacg	1080
acaaacaaga	gagcagtcaa	aataatagta	a	acactcaggt	cattaacca	ccaatagtg	1140
cgcaaaaaac	agaagttcaa	cccacgcaag	t	cattgatgg	gccttttgcg	ggcggcaaa	1200
acacggttgt	caatatcaac	cgcacgaaca	c	taacgctga	tggcacgatt	agagtgggag	1260
ggtttaaagc	ttctcttacc	accaatgcgg	c	tcatttgca	tatcggcaaa	ggcgggtgtca	1320
atctgtccaa	tcaagcgagc	gggcgctctc	t	tatagtgga	aaatctaact	gggaatatca	1380
ccgttgatgg	gcctttaaga	gtgaataatc	a	agtgggtgg	ctatgctttg	gcaggatcaa	1440
gcgcgaattt	tgagtttaag	gctgggtacg	a	tacaaaaaa	cggcacagcc	acttttaata	1500
acgatattag	tctgggaaga	tttgtgaatt	t	aaaggtgga	tgctcataca	gctaatttta	1560
aaggtattga	tacgggtaat	ggtggtttca	a	acaccttaga	ttttagtggc	gttacagaca	1620
aagtcaatat	caacaagctc	attacggctt	c	cactaatgt	ggccgttaaa	aacttcaaca	1680
ttaatgaatt	gattgttaaa	accaatggga	t	aagtgtggg	ggaatatact	catttttagcg	1740
aagatatagg	cagtcaatcg	cgcacgaata	c	cggtgcgttt	ggaaactggc	actaggtcac	1800
ttttctctgg	gggtgttaaa	tttaaagggtg	g	cgaaaaaatt	ggttatagat	gagttttact	1860
atagcccttg	gaattatttt	gacgctagaa	a	tattaaaaa	tggtgaaatc	accaataaac	1920
ttgcttttgg	acctcaagga	agtccttggg	g	cacatcaaa	acttatgttc	aataatctaa	1980
ccctagggtca	aatgcgggtc	atggattata	g	ccaatttttc	aaatttaacc	attcaagggg	2040
atttcatcaa	caatcaaggc	actatcaact	a	tctgggtccg	aggtgggaaa	gtggcaacct	2100
taagcgtagg	caatgcagca	gctatgatgt	t	taataatga	tatagacagc	gcgaccggat	2160
tttacaacc	gctcatcaag	attaacagcg	c	tcaagatct	cattaataat	acagaacatg	2220
ttttattgaa	agcgaataatc	attgggttatg	g	taatgtttc	tacaggtacc	aatggcatta	2280
gtaatgttaa	tctagaagag	caattcaaag	a	gcgcctagc	cctttataac	aacaataacc	2340
gcatggatac	ttgtgtgggtg	cgaaatactg	a	tgacattaa	agcatgcggg	atggctatcg	2400
gcgatcaaa	catgggtgaac	aaccctgaca	a	ttacaagta	tcttatcggt	aaggcatgga	2460
aaaatatagg	gatcagcaaa	acagctaata	g	ctctaaaaat	ttcgggtgtat	tatttaggca	2520
attctacgcc	tactgagaat	ggtggcaata	c	cacaaattt	accacaaaac	accactagca	2580
atgcacgttc	tgccaacaac	gcccttgac	a	aaacgctcc	tttcgctcaa	cctagtgtca	2640
ctcctaattt	agtcgctatc	aatcagcatg	a	ttttggcac	tattgaaagc	gtgtttgaat	2700
tggtcaaccg	ctctaaagat	attgacacgc	t	ttatgtctaa	ctcaggcgct	caaggcaggg	2760
atctcttaca	aaccttattg	attgatagcc	a	tgatgcggg	ttatgccaga	aaaatgattg	2820

CHIR0157 (updated 06-06-06).ST25.txt

```

atgctacaag cgctaataag atcaccaagc aattgaatac ggccactacc actttaaaca 2880
acatagccag tttagagcat aaaaccagcg gcttacaaac tttgagcttg agtaatgcga 2940
tgattttaaa ttctcgttta gtcaatctct ccaggagaca caccaaccat attgactcgt 3000
tcgccaaacg cttacaagct ttaaaagacc aaaaattcgc ttcttttagaa agcgcggcag 3060
aagtgttgta tcaatttgcc cctaaatatg aaaaacctac caatgttttg gctaacgcta 3120
ttgggggaac gagcttgaat aatggctcta acgcttcatt gtatggcaca agcgcgggag 3180
tagacgctta ccttaacggg caagtgaag ccattgtggg cggttttgga agctatggtt 3240
atagctcttt taataatcgt gcgaactccc ttaactctgg ggccaataac actaattttg 3300
gcgtgtatag ccgtattttt gccaaccagc atgaatttga ctttgaagct caaggggcac 3360
tagggagcga tcaatcaagc ttgaatttca aaagcgctct attacaagat ttgaatcaaa 3420
gctatcatta cttagcctat agcgctgcaa caagagcgag ctatggttat gacttcgcgt 3480
tttttaggaa cgcttttagt ttaaaaccaa gcgtgggtgt gagctataac catttagggt 3540
caaccaactt taaaagcaac agcaccaatc aagtggcttt gaaaaatggc tctagcagtc 3600
agcatttatt caacgctagc gctaattgtg aagcgcgcta ttattatggg gacacttcac 3660
acttctacat gaatgctgga gttttacaag agttcgctca tgttggctct aataacgccg 3720
cgtcttttaa caccttttaa gtgaatgccg ctcgcaaccc tttaaatacc catgccagag 3780
tgatgatggg tggggaatta aaattagcta aagaagtgtt tttgaatttg ggcgttggtt 3840
atgtgcacaa tttgatttcc aatataggcc atttcgcttc caatttagga atgaggtata 3900
gtttctaaat accgctctta aacccatgct caaagcatgg gtttgaaatc ttacaaaaca 3960

```

<210> 3  
 <211> 1296  
 <212> PRT  
 <213> Helicobacter pylori

<400> 3

Met Glu Ile Gln Gln Thr His Arg Lys Ile Asn Arg Pro Leu Val Ser  
 1 5 10 15

Leu Ala Leu Val Gly Ala Leu Val Ser Ile Thr Pro Gln Gln Ser His  
 20 25 30

Ala Ala Phe Phe Thr Thr Val Ile Ile Pro Ala Ile Val Gly Gly Ile  
 35 40 45

Ala Thr Gly Thr Ala Val Gly Thr Val Ser Gly Leu Leu Ser Trp Gly  
 50 55 60

Leu Lys Gln Ala Glu Glu Ala Asn Lys Thr Pro Asp Lys Pro Asp Lys  
 65 70 75 80

Val Trp Arg Ile Gln Ala Gly Lys Gly Phe Asn Glu Phe Pro Asn Lys

Glu Tyr Asp Leu Tyr Arg Ser Leu Leu Ser Ser Lys Ile Asp Gly Gly  
 100 105 110  
 Trp Asp Trp Gly Asn Ala Ala Arg His Tyr Trp Val Lys Gly Gly Gln  
 115 120 125  
 Gln Asn Lys Leu Glu Val Asp Met Lys Asp Ala Val Gly Thr Tyr Thr  
 130 135 140  
 Leu Ser Gly Leu Arg Asn Phe Thr Gly Gly Asp Leu Asp Val Asn Met  
 145 150 155 160  
 Gln Lys Ala Thr Leu Arg Leu Gly Gln Phe Asn Gly Asn Ser Phe Thr  
 165 170 175  
 Ser Tyr Lys Asp Ser Ala Asp Arg Thr Thr Arg Val Asp Phe Asn Ala  
 180 185 190  
 Lys Asn Ile Ser Ile Asp Asn Phe Val Glu Ile Asn Asn Arg Val Gly  
 195 200 205  
 Ser Gly Ala Gly Arg Lys Ala Ser Ser Thr Val Leu Thr Leu Gln Ala  
 210 215 220  
 Ser Glu Gly Ile Thr Ser Asp Lys Asn Ala Glu Ile Ser Leu Tyr Asp  
 225 230 235 240  
 Gly Ala Thr Leu Asn Leu Ala Ser Ser Ser Val Lys Leu Met Gly Asn  
 245 250 255  
 Val Trp Met Gly Arg Leu Gln Tyr Val Gly Ala Tyr Leu Ala Pro Ser  
 260 265 270  
 Tyr Ser Thr Ile Asn Thr Ser Lys Val Thr Gly Glu Val Asn Phe Asn  
 275 280 285  
 His Leu Thr Val Gly Asp Lys Asn Ala Ala Gln Ala Gly Ile Ile Ala  
 290 295 300  
 Asn Lys Lys Thr Asn Ile Gly Thr Leu Asp Leu Trp Gln Ser Ala Gly  
 305 310 315 320  
 Leu Asn Ile Ile Ala Pro Pro Glu Gly Gly Tyr Lys Asp Lys Pro Asn  
 325 330 335  
 Asn Thr Pro Ser Gln Ser Gly Ala Lys Asn Asp Lys Asn Glu Ser Ala  
 340 345 350  
 Lys Asn Asp Lys Gln Glu Ser Ser Gln Asn Asn Ser Asn Thr Gln Val

355

360

365

Ile Asn Pro Pro Asn Ser Ala Gln Lys Thr Glu Val Gln Pro Thr Gln  
 370 375 380

Val Ile Asp Gly Pro Phe Ala Gly Gly Lys Asp Thr Val Val Asn Ile  
 385 390 395 400

Asn Arg Ile Asn Thr Asn Ala Asp Gly Thr Ile Arg Val Gly Gly Phe  
 405 410 415

Lys Ala Ser Leu Thr Thr Asn Ala Ala His Leu His Ile Gly Lys Gly  
 420 425 430

Gly Val Asn Leu Ser Asn Gln Ala Ser Gly Arg Ser Leu Ile Val Glu  
 435 440 445

Asn Leu Thr Gly Asn Ile Thr Val Asp Gly Pro Leu Arg Val Asn Asn  
 450 455 460

Gln Val Gly Gly Tyr Ala Leu Ala Gly Ser Ser Ala Asn Phe Glu Phe  
 465 470 475 480

Lys Ala Gly Thr Asp Thr Lys Asn Gly Thr Ala Thr Phe Asn Asn Asp  
 485 490 495

Ile Ser Leu Gly Arg Phe Val Asn Leu Lys Val Asp Ala His Thr Ala  
 500 505 510

Asn Phe Lys Gly Ile Asp Thr Gly Asn Gly Gly Phe Asn Thr Leu Asp  
 515 520 525

Phe Ser Gly Val Thr Asp Lys Val Asn Ile Asn Lys Leu Ile Thr Ala  
 530 535 540

Ser Thr Asn Val Ala Val Lys Asn Phe Asn Ile Asn Glu Leu Ile Val  
 545 550 555 560

Lys Thr Asn Gly Ile Ser Val Gly Glu Tyr Thr His Phe Ser Glu Asp  
 565 570 575

Ile Gly Ser Gln Ser Arg Ile Asn Thr Val Arg Leu Glu Thr Gly Thr  
 580 585 590

Arg Ser Leu Phe Ser Gly Gly Val Lys Phe Lys Gly Gly Glu Lys Leu  
 595 600 605

Val Ile Asp Glu Phe Tyr Tyr Ser Pro Trp Asn Tyr Phe Asp Ala Arg  
 610 615 620

Asn Ile Lys Asn Val Glu Ile Thr Asn Lys Leu Ala Phe Gly Pro Gln

625 630 635 640

Gly Ser Pro Trp Gly Thr Ser Lys Leu Met Phe Asn Asn Leu Thr Leu  
645 650 655

Gly Gln Asn Ala Val Met Asp Tyr Ser Gln Phe Ser Asn Leu Thr Ile  
660 665 670

Gln Gly Asp Phe Ile Asn Asn Gln Gly Thr Ile Asn Tyr Leu Val Arg  
675 680 685

Gly Gly Lys Val Ala Thr Leu Ser Val Gly Asn Ala Ala Ala Met Met  
690 695 700

Phe Asn Asn Asp Ile Asp Ser Ala Thr Gly Phe Tyr Lys Pro Leu Ile  
705 710 715 720

Lys Ile Asn Ser Ala Gln Asp Leu Ile Lys Asn Thr Glu His Val Leu  
725 730 735

Leu Lys Ala Lys Ile Ile Gly Tyr Gly Asn Val Ser Thr Gly Thr Asn  
740 745 750

Gly Ile Ser Asn Val Asn Leu Glu Glu Gln Phe Lys Glu Arg Leu Ala  
755 760 765

Leu Tyr Asn Asn Asn Asn Arg Met Asp Thr Cys Val Val Arg Asn Thr  
770 775 780

Asp Asp Ile Lys Ala Cys Gly Met Ala Ile Gly Asp Gln Ser Met Val  
785 790 795 800

Asn Asn Pro Asp Asn Tyr Lys Tyr Leu Ile Gly Lys Ala Trp Lys Asn  
805 810 815

Ile Gly Ile Ser Lys Thr Ala Asn Gly Ser Lys Ile Ser Val Tyr Tyr  
820 825 830

Leu Gly Asn Ser Thr Pro Thr Glu Asn Gly Gly Asn Thr Thr Asn Leu  
835 840 845

Pro Thr Asn Thr Thr Ser Asn Ala Arg Ser Ala Asn Asn Ala Leu Ala  
850 855 860

Gln Asn Ala Pro Phe Ala Gln Pro Ser Ala Thr Pro Asn Leu Val Ala  
865 870 875 880

Ile Asn Gln His Asp Phe Gly Thr Ile Glu Ser Val Phe Glu Leu Ala  
885 890 895

Asn Arg Ser Lys Asp Ile Asp Thr Leu Tyr Ala Asn Ser Gly Ala Gln  
Page 6

900

905

910

Gly Arg Asp Leu Leu Gln Thr Leu Leu Ile Asp Ser His Asp Ala Gly  
 915 920 925  
 Tyr Ala Arg Lys Met Ile Asp Ala Thr Ser Ala Asn Glu Ile Thr Lys  
 930 935 940  
 Gln Leu Asn Thr Ala Thr Thr Thr Leu Asn Asn Ile Ala Ser Leu Glu  
 945 950 955 960  
 His Lys Thr Ser Gly Leu Gln Thr Leu Ser Leu Ser Asn Ala Met Ile  
 965 970 975  
 Leu Asn Ser Arg Leu Val Asn Leu Ser Arg Arg His Thr Asn His Ile  
 980 985 990  
 Asp Ser Phe Ala Lys Arg Leu Gln Ala Leu Lys Asp Gln Lys Phe Ala  
 995 1000 1005  
 Ser Leu Glu Ser Ala Ala Glu Val Leu Tyr Gln Phe Ala Pro Lys  
 1010 1015 1020  
 Tyr Glu Lys Pro Thr Asn Val Trp Ala Asn Ala Ile Gly Gly Thr  
 1025 1030 1035  
 Ser Leu Asn Asn Gly Ser Asn Ala Ser Leu Tyr Gly Thr Ser Ala  
 1040 1045 1050  
 Gly Val Asp Ala Tyr Leu Asn Gly Gln Val Glu Ala Ile Val Gly  
 1055 1060 1065  
 Gly Phe Gly Ser Tyr Gly Tyr Ser Ser Phe Asn Asn Arg Ala Asn  
 1070 1075 1080  
 Ser Leu Asn Ser Gly Ala Asn Asn Thr Asn Phe Gly Val Tyr Ser  
 1085 1090 1095  
 Arg Ile Phe Ala Asn Gln His Glu Phe Asp Phe Glu Ala Gln Gly  
 1100 1105 1110  
 Ala Leu Gly Ser Asp Gln Ser Ser Leu Asn Phe Lys Ser Ala Leu  
 1115 1120 1125  
 Leu Gln Asp Leu Asn Gln Ser Tyr His Tyr Leu Ala Tyr Ser Ala  
 1130 1135 1140  
 Ala Thr Arg Ala Ser Tyr Gly Tyr Asp Phe Ala Phe Phe Arg Asn  
 1145 1150 1155  
 Ala Leu Val Leu Lys Pro Ser Val Gly Val Ser Tyr Asn His Leu

1160

1165

1170

Gly Ser Thr Asn Phe Lys Ser Asn Ser Thr Asn Gln Val Ala Leu  
1175 1180 1185

Lys Asn Gly Ser Ser Ser Gln His Leu Phe Asn Ala Ser Ala Asn  
1190 1195 1200

Val Glu Ala Arg Tyr Tyr Tyr Gly Asp Thr Ser Tyr Phe Tyr Met  
1205 1210 1215

Asn Ala Gly Val Leu Gln Glu Phe Ala His Val Gly Ser Asn Asn  
1220 1225 1230

Ala Ala Ser Leu Asn Thr Phe Lys Val Asn Ala Ala Arg Asn Pro  
1235 1240 1245

Leu Asn Thr His Ala Arg Val Met Met Gly Gly Glu Leu Lys Leu  
1250 1255 1260

Ala Lys Glu Val Phe Leu Asn Leu Gly Val Val Tyr Leu His Asn  
1265 1270 1275

Leu Ile Ser Asn Ile Gly His Phe Ala Ser Asn Leu Gly Met Arg  
1280 1285 1290

Tyr Ser Phe  
1295

<210> 4  
<211> 5925  
<212> DNA  
<213> Helicobacter pylori

<400> 4  
ctccatttta agcaactcca tagaccacta aagaaacttt ttttgaggct atctttgaaa 60  
atctgtccta ttgatttggt ttccattttg tttcccatgt ggatcttggt gatcacaac 120  
gcttaattat acatgctata gtaagcatga cacacaaacc aaactatttt tagaacgctt 180  
catgtgctca ccttgactaa ccatttctcc aaccatactt tagcggtgca tttgatttct 240  
tcaaaaagat tcatttctta tttcttggtc ttattaaagt tctttcattt tagcaaattt 300  
ttgttaattg tgggtaaaaa tgtgaatcgt cctagccttt agacgcctgc aacgatcggg 360  
cttttttcaa tattaataat gattaatgaa aaaaaaaaaa aatgcttgat attgttgat 420  
aatgagaatg ttcaaagaca tgaattgact actcaagcgt gtagcgattt ttagcagtct 480  
ttgacactaa caagataccg ataggatga aactaggtat agtaaggaga aacaatgact 540  
aacgaaacca ttgaccaaca accacaaacc gaagcggctt ttaacccgca gcaatttatc 600  
aataatcttc aagtagcttt tcttaaagtt gataacgctg tcgcttcata cgatcctgat 660  
caaaaaccaa tcgttgataa gaacgatagg gataacaggc aagcttttga aggaatctcg 720



## CHIR0157 (updated 06-06-06).ST25.txt

caattaaggg	aagaatactc	caataaagcg	atcaaaaatc	ctaccaaaaa	gaatcagtat	780
ttttcagact	ttatcaataa	gagcaatgat	ttaatcaaca	aagacaatct	cattgatgta	840
gaatcttcca	caaagagctt	tcagaaatth	ggggatcagc	gttaccgaat	tttcacaagt	900
tgggtgtccc	atcaaaacga	tccgtctaaa	atcaacaccc	gatcgatccg	aaatthttatg	960
gaaaatatca	tacaaccccc	tatccttgat	gataaagaga	aagcggagtt	tttgaaatct	1020
gccaaacaat	cttttgagc	aatcattata	gggaatcaaa	tccgaacgga	tcaaaagttc	1080
atgggcgtgt	ttgatgagtc	cttgaaagaa	aggcaagaag	cagaaaaaaa	tggagagcct	1140
actggtgggg	attggttggg	tattthttctc	tcatthttat	ttgacaaaaa	acaatcttct	1200
gatgtcaaa	aagcaatcaa	tcaagaacca	gttccccatg	tccaaccaga	tatagccact	1260
accaccaccg	acatacaagg	cttaccgcct	gaagctagag	atttacttga	tgaaaggggt	1320
aattthttcta	aattcactct	tggcgatatg	gaaatgttag	atgttgaggg	agtcgctgac	1380
attgatccca	attacaagtt	caatcaatta	ttgattcaca	ataacgctct	gtcttctgtg	1440
ttaatgggga	gtcataatgg	catagaacct	gaaaaagttt	cattgttgta	tgggggcaat	1500
ggtggtcctg	gagctaggca	tgattggaac	gccaccgttg	gttataaaga	ccaacaaggc	1560
aacaatgtgg	ctacaataat	taatgtgcat	atgaaaaacg	gcagtggctt	agtcatagca	1620
ggtggtgaga	aagggattaa	caaccctagt	ttttatctct	acaaagaaga	ccaactcaca	1680
ggctcacaac	gagcattaag	tcaagaagag	atccaaaaca	aatagatttt	catggaattt	1740
cttgcacaaa	ataatgctaa	attagacaac	ttgagcgaga	aagagaagga	aaaattccga	1800
actgagatta	aagattttcca	aaaagactct	aaggcttatt	tagacgccct	agggaatgat	1860
cgtatttgctt	ttgtttctaa	aaaagacaca	aaacattcag	ctttaattac	tgagtttggt	1920
aatggggatt	tgagctacac	tctcaaagat	tatgggaaaa	aagcagataa	agcttttagat	1980
agggagaaaa	atgttactct	tcaaggtagc	ctaaaacatg	atggcgatg	gtttgttgat	2040
tatttctaatt	tcaaatacac	caacgcctcc	aagaatccca	ataagggtgt	aggcgttacg	2100
aatggcgttt	cccattttaga	agtaggcttt	aacaaggtag	ctatctttta	tttgcctgat	2160
ttaaataatc	tcgctatcac	tagtttcgta	aggcggaatt	tagaggataa	actaaccact	2220
aaaggattgt	ccccacaaga	agctaataag	cttatcaaag	atthtttgag	cagcaacaaa	2280
gaattgggtg	gaaaaacttt	aaacttcaat	aaagctgtag	ctgacgctaa	aaacacaggc	2340
aattatgatg	aagtgaaaaa	agctcagaaa	gatcttgaaa	aatctctaag	gaaacgagag	2400
catttagaga	aagaagtaga	gaaaaaattg	gagagcaaaa	gcggcaacaa	aaataaaatg	2460
gaagcaaaag	ctcaagctaa	cagccaaaaa	gatgagattt	ttgcgttgat	caataaagag	2520
gctaatagag	acgcaagagc	aatcgcttac	gctcagaatc	ttaaaggcat	caaaagggaa	2580
ttgtctgata	aacttgaaaa	tgtcaacaag	aatttgaaag	actttgataa	atctthttgat	2640
gaattcaaaa	atggcaaaaa	taaggatttc	agcaaggcag	aagaaacact	aaaagccctt	2700
aaaggttcgg	tgaaagattt	aggtatcaat	ccagaatgga	tttcaaaagt	tgaaaacctt	2760

## CHIR0157 (updated 06-06-06).ST25.txt

aatgcagctt tgaatgaatt caaaaatggc aaaaataagg atttcagcaa ggtaacgcaa	2820
gcaaaaagcg accttgaaaa ttccgttaaa gatgtgatca tcaatcaaaa ggtaacggat	2880
aaagttgata atctcaatca agcggatatca gtggctaaag caacgggtga tttcagtagg	2940
gtagagcaag cgtagccga tctcaaaaat ttctcaaagg agcaattggc ccaacaagct	3000
caaaaaaatg aaagtctcaa tgctagaaaa aaatctgaaa tatatcaatc cgtaagaat	3060
ggtgtgaatg gaaccctagt cggtaatggg ttatctcaag cagaagccac aactctttct	3120
aaaaactttt cggacatcaa gaaagagttg aatgcaaaac ttggaaattt caataacaat	3180
aacaataatg gactcaaaaa cgaaccatt tatgctaaag ttaataaaaa gaaagcaggg	3240
caagcagcta gccttgaaga acccatttac gctcaagttg ctaaaaaggt aaatgcaaaa	3300
attgaccgac tcaatcaaat agcaagtggg ttgggtgttg tagggcaagc agcgggcttc	3360
cctttgaaaa ggcattgataa agttgatgat ctacagtaagg tagggctttc aaggaatcaa	3420
gaattggctc agaaaattga caatctcaat caagcgggat cagaagctaa agcaggtttt	3480
tttggcaatc tagagcaaac gatagacaag ctcaaagatt ctacaaaaca caatcccatg	3540
aatctatggg ttgaaagtgc aaaaaaagta cctgctagtt tgtcagcgaa actagacaat	3600
tacgctacta acagccacat acgcattaat agcaatatca aaaatggagc aatcaatgaa	3660
aaagcgaccg gcatgctaac gcaaaaaaac cctgagtggc tcaagctcgt gaatgataag	3720
atagttgcgc ataattgtagg aagcgttcct ttgtcagagt atgataaaat tggcttcaac	3780
cagaagaata tgaaagatta ttctgattcg ttcaagtttt ccaccaagtt gaacaatgct	3840
gtaaaagaca ctaattctgg ctttacgcaa tttttaacca atgcattttc tacagcatct	3900
tattactgct tggcgagaga aaatgcggag catggaatca agaacgttaa tacaaaaggt	3960
ggtttccaaa aatcttaaag gattaaggaa taccaaaaac gcaaaaacca ccccttgcta	4020
aaagcgaggg gttttttaat actccttagc agaaatccca atcgtcttta gtatttgga	4080
tgaatgctac caattcatgg tatcatatcc ccatacttc gtatctagcg taggaagtgt	4140
gcaaagttac gcctttggag atatgatgtg tgagacctgt aggggaatgcg ttggagctca	4200
aactctgtaa aatccctatt atagggacac agagtgagaa ccaaactctc cctacgggca	4260
acatcagcct aggaagccca atcgtcttta gcggttgggc acttcacctt aaaatatccc	4320
gacagacact aacgaaaggc tttgttcttt aaagtctgca tggatatattc ctaccccaa	4380
aagacttaac cctttgctta aaattaagtt tgattgtgct agtgggttcg tgctatagt	4440
cgaaaattaa ttaagggtta taaagagagc ataaactaga aaaaacaagt agctataaca	4500
aagatcaagt tcaaaaaatc atagagcttt tagagcaaat tgatcgcgct ctaaccaa	4560
gaaaaatcag aaaaaccata ggaattatca caccttataa tgcccaaaaa agacgcttgc	4620
gatcagaagt ggaaaaatac ggcttcaaga attttgatga gctcaaaata gacactgtgg	4680
atgcctttca aggtgaagag gcagatatta ttatttattc caccgtgaaa acttggtgta	4740
atctttcttt cttgctagat tctaaacgct tgaatgtggc tatttctagg gcaaaagaaa	4800

CHIR0157 (updated 06-06-06).ST25.txt

```

atctcatttt tgtgggtaaa aagtcctttct ttgagaattt atgaagcgat gagaagaata 4860
tcttttagcgc tattttgcaa gtctgtagat aggtaatctt ttccaaagat aatcattaga 4920
cattcttcgc ttcaaaacgc tttcataaat ctctctaaag cgctttataa tcaacacaat 4980
acccttatag tgtgagctat agcccccttt ttgggaattga gttattttga ctttaaattt 5040
ttattagcgt tacaatttga gccattcttt agcttggttt tctagccaga tcacatcgcc 5100
gctcgcatga aattccactt tagggaatgc gtgtgcattt tttttaaggg cgtatttttg 5160
ctgcaaatat cctacaatag catcgcccga atggatgagt aggggggggtg ttgaaagggc 5220
aaaatgctcc ataaaatagc cctcaatttt ttgagcgatt aaggggaaaat gcgtgcaacc 5280
taaaataatc acttcgggaa aatctttaag ggagtgaaat aataacgcat gcaagtttct 5340
aacaattcgc cctctaaaat actttcttca atcaaaggca caaaaagaga agtggctaaa 5400
tgcgaaacat tcaaatagcc ttgttgtttc agggcattgt cataagcgtt ggattggatc 5460
gtcgtttttg tccctagcac taaaataggg gcgtttttat cttttacttg tcgcttgatc 5520
gctaaaatgc ttggctcaat cagccccaca atagggaattt tggaatgctt ttgcatctct 5580
tctaaagcta gagcgctcgc tgtgttgcat gccacaatca ataattcaat ctggtgcggt 5640
ttgaaaaaat ccaaagcctc taagccaaat tgcttgatcg tagtggggtc tttagtcca 5700
taaggcactc tagccgtatc gccataatag atgatttcat caaataattg cgcttttaaa 5760
aggcttttta aaacgctaaa ccctcccaca ccgctatcaa aaacgcctat tttcatgaca 5820
cttttttaat ttaatgggat taattaggga ttttattttt cattcattaa gtttaaaaat 5880
tcttcattgt ccttagtttg ttgcatttta gaatagacaa agctt 5925

```

<210> 5  
 <211> 1147  
 <212> PRT  
 <213> Helicobacter pylori

<400> 5

Met Thr Asn Glu Thr Ile Asp Gln Gln Pro Gln Thr Glu Ala Ala Phe  
 1 5 10 15

Asn Pro Gln Gln Phe Ile Asn Asn Leu Gln Val Ala Phe Leu Lys Val  
 20 25 30

Asp Asn Ala Val Ala Ser Tyr Asp Pro Asp Gln Lys Pro Ile Val Asp  
 35 40 45

Lys Asn Asp Arg Asp Asn Arg Gln Ala Phe Glu Gly Ile Ser Gln Leu  
 50 55 60

Arg Glu Glu Tyr Ser Asn Lys Ala Ile Lys Asn Pro Thr Lys Lys Asn  
 65 70 75 80

Gln Tyr Phe Ser Asp Phe Ile Asn Lys Ser Asn Asp Leu Ile Asn Lys  
 Page 11

Asp Asn Leu Ile Asp Val Glu Ser Ser Thr Lys Ser Phe Gln Lys Phe  
 100 105 110

Gly Asp Gln Arg Tyr Arg Ile Phe Thr Ser Trp Val Ser His Gln Asn  
 115 120 125

Asp Pro Ser Lys Ile Asn Thr Arg Ser Ile Arg Asn Phe Met Glu Asn  
 130 135 140

Ile Ile Gln Pro Pro Ile Leu Asp Asp Lys Glu Lys Ala Glu Phe Leu  
 145 150 155 160

Lys Ser Ala Lys Gln Ser Phe Ala Gly Ile Ile Ile Gly Asn Gln Ile  
 165 170 175

Arg Thr Asp Gln Lys Phe Met Gly Val Phe Asp Glu Ser Leu Lys Glu  
 180 185 190

Arg Gln Glu Ala Glu Lys Asn Gly Glu Pro Thr Gly Gly Asp Trp Leu  
 195 200 205

Asp Ile Phe Leu Ser Phe Ile Phe Asp Lys Lys Gln Ser Ser Asp Val  
 210 215 220

Lys Glu Ala Ile Asn Gln Glu Pro Val Pro His Val Gln Pro Asp Ile  
 225 230 235 240

Ala Thr Thr Thr Thr Asp Ile Gln Gly Leu Pro Pro Glu Ala Arg Asp  
 245 250 255

Leu Leu Asp Glu Arg Gly Asn Phe Ser Lys Phe Thr Leu Gly Asp Met  
 260 265 270

Glu Met Leu Asp Val Glu Gly Val Ala Asp Ile Asp Pro Asn Tyr Lys  
 275 280 285

Phe Asn Gln Leu Leu Ile His Asn Asn Ala Leu Ser Ser Val Leu Met  
 290 295 300

Gly Ser His Asn Gly Ile Glu Pro Glu Lys Val Ser Leu Leu Tyr Gly  
 305 310 315 320

Gly Asn Gly Gly Pro Gly Ala Arg His Asp Trp Asn Ala Thr Val Gly  
 325 330 335

Tyr Lys Asp Gln Gln Gly Asn Asn Val Ala Thr Ile Ile Asn Val His  
 340 345 350

Met Lys Asn Gly Ser Gly Leu Val Ile Ala Gly Gly Glu Lys Gly Ile  
 Page 12

355

360

365

Asn Asn Pro Ser Phe Tyr Leu Tyr Lys Glu Asp Gln Leu Thr Gly Ser  
 370 375 380

Gln Arg Ala Leu Ser Gln Glu Glu Ile Gln Asn Lys Ile Asp Phe Met  
 385 390 395 400

Glu Phe Leu Ala Gln Asn Asn Ala Lys Leu Asp Asn Leu Ser Glu Lys  
 405 410 415

Glu Lys Glu Lys Phe Arg Thr Glu Ile Lys Asp Phe Gln Lys Asp Ser  
 420 425 430

Lys Ala Tyr Leu Asp Ala Leu Gly Asn Asp Arg Ile Ala Phe Val Ser  
 435 440 445

Lys Lys Asp Thr Lys His Ser Ala Leu Ile Thr Glu Phe Gly Asn Gly  
 450 455 460

Asp Leu Ser Tyr Thr Leu Lys Asp Tyr Gly Lys Lys Ala Asp Lys Ala  
 465 470 475 480

Leu Asp Arg Glu Lys Asn Val Thr Leu Gln Gly Ser Leu Lys His Asp  
 485 490 495

Gly Val Met Phe Val Asp Tyr Ser Asn Phe Lys Tyr Thr Asn Ala Ser  
 500 505 510

Lys Asn Pro Asn Lys Gly Val Gly Val Thr Asn Gly Val Ser His Leu  
 515 520 525

Glu Val Gly Phe Asn Lys Val Ala Ile Phe Asn Leu Pro Asp Leu Asn  
 530 535 540

Asn Leu Ala Ile Thr Ser Phe Val Arg Arg Asn Leu Glu Asp Lys Leu  
 545 550 555 560

Thr Thr Lys Gly Leu Ser Pro Gln Glu Ala Asn Lys Leu Ile Lys Asp  
 565 570 575

Phe Leu Ser Ser Asn Lys Glu Leu Val Gly Lys Thr Leu Asn Phe Asn  
 580 585 590

Lys Ala Val Ala Asp Ala Lys Asn Thr Gly Asn Tyr Asp Glu Val Lys  
 595 600 605

Lys Ala Gln Lys Asp Leu Glu Lys Ser Leu Arg Lys Arg Glu His Leu  
 610 615 620

Glu Lys Glu Val Glu Lys Lys Leu Glu Ser Lys Ser Gly Asn Lys Asn  
 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995

625 630 635 640

Lys Met Glu Ala Lys Ala Gln Ala Asn Ser Gln Lys Asp Glu Ile Phe  
645 650 655

Ala Leu Ile Asn Lys Glu Ala Asn Arg Asp Ala Arg Ala Ile Ala Tyr  
660 665 670

Ala Gln Asn Leu Lys Gly Ile Lys Arg Glu Leu Ser Asp Lys Leu Glu  
675 680 685

Asn Val Asn Lys Asn Leu Lys Asp Phe Asp Lys Ser Phe Asp Glu Phe  
690 695 700

Lys Asn Gly Lys Asn Lys Asp Phe Ser Lys Ala Glu Glu Thr Leu Lys  
705 710 715 720

Ala Leu Lys Gly Ser Val Lys Asp Leu Gly Ile Asn Pro Glu Trp Ile  
725 730 735

Ser Lys Val Glu Asn Leu Asn Ala Ala Leu Asn Glu Phe Lys Asn Gly  
740 745 750

Lys Asn Lys Asp Phe Ser Lys Val Thr Gln Ala Lys Ser Asp Leu Glu  
755 760 765

Asn Ser Val Lys Asp Val Ile Ile Asn Gln Lys Val Thr Asp Lys Val  
770 775 780

Asp Asn Leu Asn Gln Ala Val Ser Val Ala Lys Ala Thr Gly Asp Phe  
785 790 795 800

Ser Arg Val Glu Gln Ala Leu Ala Asp Leu Lys Asn Phe Ser Lys Glu  
805 810 815

Gln Leu Ala Gln Gln Ala Gln Lys Asn Glu Ser Leu Asn Ala Arg Lys  
820 825 830

Lys Ser Glu Ile Tyr Gln Ser Val Lys Asn Gly Val Asn Gly Thr Leu  
835 840 845

Val Gly Asn Gly Leu Ser Gln Ala Glu Ala Thr Thr Leu Ser Lys Asn  
850 855 860

Phe Ser Asp Ile Lys Lys Glu Leu Asn Ala Lys Leu Gly Asn Phe Asn  
865 870 875 880

Asn Asn Asn Asn Asn Gly Leu Lys Asn Glu Pro Ile Tyr Ala Lys Val  
885 890 895

Asn Lys Lys Lys Ala Gly Gln Ala Ala Ser Leu Glu Glu Pro Ile Tyr  
Page 14

900

905

910

Ala Gln Val Ala Lys Lys Val Asn Ala Lys Ile Asp Arg Leu Asn Gln  
 915 920 925

Ile Ala Ser Gly Leu Gly Val Val Gly Gln Ala Ala Gly Phe Pro Leu  
 930 935 940

Lys Arg His Asp Lys Val Asp Asp Leu Ser Lys Val Gly Leu Ser Arg  
 945 950 955 960

Asn Gln Glu Leu Ala Gln Lys Ile Asp Asn Leu Asn Gln Ala Val Ser  
 965 970 975

Glu Ala Lys Ala Gly Phe Phe Gly Asn Leu Glu Gln Thr Ile Asp Lys  
 980 985 990

Leu Lys Asp Ser Thr Lys His Asn Pro Met Asn Leu Trp Val Glu Ser  
 995 1000 1005

Ala Lys Lys Val Pro Ala Ser Leu Ser Ala Lys Leu Asp Asn Tyr  
 1010 1015 1020

Ala Thr Asn Ser His Ile Arg Ile Asn Ser Asn Ile Lys Asn Gly  
 1025 1030 1035

Ala Ile Asn Glu Lys Ala Thr Gly Met Leu Thr Gln Lys Asn Pro  
 1040 1045 1050

Glu Trp Leu Lys Leu Val Asn Asp Lys Ile Val Ala His Asn Val  
 1055 1060 1065

Gly Ser Val Pro Leu Ser Glu Tyr Asp Lys Ile Gly Phe Asn Gln  
 1070 1075 1080

Lys Asn Met Lys Asp Tyr Ser Asp Ser Phe Lys Phe Ser Thr Lys  
 1085 1090 1095

Leu Asn Asn Ala Val Lys Asp Thr Asn Ser Gly Phe Thr Gln Phe  
 1100 1105 1110

Leu Thr Asn Ala Phe Ser Thr Ala Ser Tyr Tyr Cys Leu Ala Arg  
 1115 1120 1125

Glu Asn Ala Glu His Gly Ile Lys Asn Val Asn Thr Lys Gly Gly  
 1130 1135 1140

Phe Gln Lys Ser  
 1145

&lt;210&gt; 6

&lt;211&gt; 546

&lt;212&gt; PRT

&lt;213&gt; Helicobacter pylori

&lt;400&gt; 6

Met Ala Lys Glu Ile Lys Phe Ser Asp Ser Ala Arg Asn Leu Leu Phe  
 1 5 10 15

Glu Gly Val Arg Gln Leu His Asp Ala Val Lys Val Thr Met Gly Pro  
 20 25 30

Arg Gly Arg Asn Val Leu Ile Gln Lys Ser Tyr Gly Ala Pro Ser Ile  
 35 40 45

Thr Lys Asp Gly Val Ser Val Ala Lys Glu Ile Glu Leu Ser Cys Pro  
 50 55 60

Val Ala Asn Met Gly Ala Gln Leu Val Lys Glu Val Ala Ser Lys Thr  
 65 70 75 80

Ala Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Tyr  
 85 90 95

Ser Ile Phe Lys Glu Gly Leu Arg Asn Ile Thr Ala Gly Ala Asn Pro  
 100 105 110

Ile Glu Val Lys Arg Gly Met Asp Lys Ala Ala Glu Ala Ile Ile Asn  
 115 120 125

Glu Leu Lys Lys Ala Ser Lys Lys Val Gly Gly Lys Glu Glu Ile Thr  
 130 135 140

Gln Val Ala Thr Ile Ser Ala Asn Ser Asp His Asn Ile Gly Lys Leu  
 145 150 155 160

Ile Ala Asp Ala Met Glu Lys Val Gly Lys Asp Gly Val Ile Thr Val  
 165 170 175

Glu Glu Ala Lys Gly Ile Glu Asp Glu Leu Asp Val Val Glu Gly Met  
 180 185 190

Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe Val Thr Asn Ala Glu  
 195 200 205

Lys Met Thr Ala Gln Leu Asp Asn Ala Tyr Ile Leu Leu Thr Asp Lys  
 210 215 220

Lys Ile Ser Ser Met Lys Asp Ile Leu Pro Leu Leu Glu Lys Thr Met  
 225 230 235 240

Lys Glu Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Ile Glu Gly Glu  
 245 250 255



CHIR0157 (updated 06-06-06).ST25.txt

Ala Leu Thr Thr Leu Val Val Asn Lys Leu Arg Gly Val Leu Asn Ile  
260 265 270

Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Glu Met Leu  
275 280 285

Lys Asp Ile Ala Ile Leu Thr Gly Gly Gln Val Ile Ser Glu Glu Leu  
290 295 300

Gly Leu Ser Leu Glu Asn Ala Glu Val Glu Phe Leu Gly Lys Ala Gly  
305 310 315 320

Arg Ile Val Ile Asp Lys Asp Asn Thr Thr Ile Val Asp Gly Lys Gly  
325 330 335

His Ser Asp Asp Val Lys Asp Arg Val Ala Gln Ile Lys Thr Gln Ile  
340 345 350

Ala Ser Thr Thr Ser Asp Tyr Asp Lys Glu Lys Leu Gln Glu Arg Leu  
355 360 365

Ala Lys Leu Ser Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala Ser  
370 375 380

Glu Val Glu Met Lys Glu Lys Lys Asp Arg Val Asp Asp Ala Leu Ser  
385 390 395 400

Ala Thr Lys Ala Ala Val Glu Glu Gly Ile Val Ile Gly Gly Gly Ala  
405 410 415

Ala Leu Ile Arg Ala Ala Gln Lys Val His Leu Asn Leu His Asp Asp  
420 425 430

Glu Lys Val Gly Tyr Glu Ile Ile Met Arg Ala Ile Lys Ala Pro Leu  
435 440 445

Ala Gln Ile Ala Ile Asn Ala Gly Tyr Asp Gly Gly Val Val Val Asn  
450 455 460

Glu Val Glu Lys His Glu Gly His Phe Gly Phe Asn Ala Ser Asn Gly  
465 470 475 480

Lys Tyr Val Asp Met Phe Lys Glu Gly Ile Ile Asp Pro Leu Lys Val  
485 490 495

Glu Arg Ile Ala Leu Gln Asn Ala Val Ser Val Ser Ser Leu Leu Leu  
500 505 510

Thr Thr Glu Ala Thr Val His Glu Ile Lys Glu Glu Lys Ala Thr Pro  
515 520 525

## CHIR0157 (updated 06-06-06).ST25.txt

Ala Met Pro Asp Met Gly Gly Met Gly Gly Met Gly Gly Met Gly Gly  
 530 535 540

Met Met  
 545

<210> 7  
 <211> 1838  
 <212> DNA  
 <213> Helicobacter pylori

<400> 7  
 aagcttgctg tcatgatcac aaaaaacact aaaaaacatt attattaagg atacaaaatg 60  
 gcaaaagaaa tcaaattttc agatagtgcg agaaaccttt tatttgaagg cgtgaggcaa 120  
 ctccatgacg ctgtcaaagt aaccatgggg ccaagaggca ggaatgtatt gatccaaaaa 180  
 agctatggcg ctccaagcat caccaaagac ggcgtgagcg tggctaaaga gattgaatta 240  
 agttgcccag tagctaacat gggcgctcaa ctcgttaaag aagtagcgag caaaaccgct 300  
 gatgctgccg gcgatggcac gaccacagcg accgtgctag cttatagcat ttttaaagaa 360  
 ggtttgagga atatcacggc tggggctaac cctattgaag tgaaacgagg catggataaa 420  
 gctgctgaag cgatcattaa tgagcttaaa aaagcgagca aaaaagtagg cggtaaagaa 480  
 gaaatcacc aagtggcgac ctttctgca aactccgac acaatatcgg gaaactcatc 540  
 gctgacgcta tggaaaaagt gggtaaagac ggcgtgatca ccgttgagga agctaagggc 600  
 attgaagatg aattggatgt cgtagaaggc atgcaatttg atagaggcta cctctcccct 660  
 tattttgtaa cgaacgctga gaaaatgacc gctcaatttg ataattgctta catcctttta 720  
 acggataaaa aaatctctag catgaaagac attctcccg tactagaaaa aaccatgaaa 780  
 gagggcaaac cgcttttaat catcgctgaa gacattgagg gcgaagcttt aacgactcta 840  
 gtggtgaata aattaagagg cgtgttgaat atcgagcggt ttaaagctcc aggctttggg 900  
 gacagaagaa aagaaatgct caaagacatc gctattttta cggcggtca agtcattagc 960  
 gaagaattgg gcttgagtct agaaaacgct gaagtggagt ttttaggcaa agctggaagg 1020  
 attgtgattg acaaagacaa caccacgac gtagatggca aaggccatag cgatgatgtt 1080  
 aaagacagag tcgcgagat caaaacccaa attgcaagta cgacaagcga ttatgacaaa 1140  
 gaaaaattgc aagaaagatt ggctaaactc tctggcggtg tggctgtgat taaagtgggc 1200  
 gctgagagtg aagtggaaat gaaagagaaa aaagaccggg tggatgacgc gttgagcgcg 1260  
 actaaagcgg cggttgaaga aggcattgtg attggtggcg gtgcggctct cattcgcgcg 1320  
 gctcaaaaag tgcatttgaa ttgacgat gatgaaaaag tgggctatga aatcatcatg 1380  
 cgcgccatta aagccccatt agctcaaac gctatcaac ctggttatga tggcggtgtg 1440  
 gtcgtgaatg aagtagaaaa acacgaaggg cattttggtt ttaacgctag caatggcaag 1500  
 tatgtggata tgtttaaaga aggcattatt gacccttaa aagtagaaag gatcgctcta 1560

CHIR0157 (updated 06-06-06).ST25.txt

caaaatgcgg tttcggtttc aagcctgctt ttaaccacag aagccaccgt gcatgaaatc 1620  
aaagaagaaa aagcgactcc ggcaatgcct gatatgggtg gcatgggcgg tatgggaggc 1680  
atgggcggca tgatgtaagc ccgcttgctt tttagtataa tctgctttta aaatcccttc 1740  
tctaaatccc cccctttcta aaatctcttt tttggggggg tgctttgata aaaccgctcg 1800  
cttgtaaaaa catgcaacaa aaaatctctg ttaagctt 1838

<210> 8  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer oligonucleotide

<400> 8  
gactcgagtc gacatcga 18

<210> 9  
<211> 12  
<212> PRT  
<213> Helicobacter pylori

<400> 9  
Glu Phe Lys Asn Gly Lys Asn Lys Asp Phe Ser Lys  
1 5 10

<210> 10  
<211> 5  
<212> PRT  
<213> Helicobacter pylori

<400> 10  
Glu Pro Ile Tyr Ala  
1 5

<210> 11  
<211> 102  
<212> DNA  
<213> Helicobacter pylori

<400> 11  
gggcgatcgg ttagccctga acccatttat gctacgattg atgatctccg gcggaccttt 60  
ccctttgaaa ggcataataa agttgatgat ctcaagtaagg ta 102

<210> 12  
<211> 34  
<212> PRT  
<213> Helicobacter pylori

<400> 12  
Gly Arg Ser Val Ser Pro Glu Pro Ile Tyr Ala Thr Ile Asp Asp Leu  
1 5 10 15

Gly Gly Pro Phe Pro Leu Lys Arg His Asp Lys Val Asp Asp Leu Ser  
Page 19

Lys Val

<210> 13  
 <211> 18  
 <212> DNA  
 <213> Helicobacter pylori

<400> 13  
 cctgaaccca tttatgct

18

<210> 14  
 <211> 6  
 <212> PRT  
 <213> Helicobacter pylori

<400> 14

Pro Glu Pro Ile Tyr Ala  
 1 5

<210> 15  
 <211> 9  
 <212> DNA  
 <213> Helicobacter pylori

<400> 15  
 gatgatctc

9

<210> 16  
 <211> 3  
 <212> PRT  
 <213> Helicobacter pylori

<400> 16

Asp Asp Leu  
 1

<210> 17  
 <211> 15  
 <212> PRT  
 <213> Helicobacter pylori

<400> 17

Phe Pro Leu Lys Arg His Asp Lys Val Asp Asp Leu Ser Lys Val  
 1 5 10 15

<210> 18  
 <211> 45  
 <212> DNA  
 <213> Helicobacter pylori

<400> 18  
 tttccctttg aaaggcata taaagttgat gatctcagta aggta

45

<210> 19

CHIR0157 (updated 06-06-06).ST25.txt

<211> 36  
 <212> DNA  
 <213> Helicobacter pylori  
 <400> 19  
 gaattcaaaa atggcaaaaa taaggatttc agcaag 36

<210> 20  
 <211> 15  
 <212> DNA  
 <213> Helicobacter pylori  
 <400> 20  
 gaaccattt atgct 15

<210> 21  
 <211> 15  
 <212> DNA  
 <213> Helicobacter pylori  
 <400> 21  
 gaaccattt acgct 15

<210> 22  
 <211> 45  
 <212> DNA  
 <213> Helicobacter pylori  
 <400> 22  
 ttccctttga aaaggcatga taaagttgat gatctcagta aggta 45

<210> 23  
 <211> 6  
 <212> PRT  
 <213> Helicobacter pylori  
 <400> 23

Asn Asn Asn Asn Asn Asn  
 1 5

<210> 24  
 <211> 18  
 <212> DNA  
 <213> Helicobacter pylori  
 <400> 24  
 aataacaata acaataat 18

<210> 25  
 <211> 228  
 <212> PRT  
 <213> Helicobacter pylori  
 <400> 25  
 Lys Asn Gly Lys Asn Lys Asp Phe Ser Lys Val Thr Gln Ala Lys Ser  
 1 5 10 15

Asp Leu Glu Asn Ser Val Lys Asp Val Ile Ile Asn Gln Lys Val Thr  
 20 25 30

CHIR0157 (updated 06-06-06).ST25.txt

Asp Lys Val Asp Asn Leu Asn Gln Ala Val Ser Val Ala Lys Ala Thr  
35 40 45

Gly Asp Phe Ser Arg Val Glu Gln Ala Leu Ala Asp Leu Lys Asn Phe  
50 55 60

Ser Lys Glu Gln Leu Ala Gln Gln Ala Gln Lys Asn Glu Ser Leu Asn  
65 70 75 80

Ala Arg Lys Lys Ser Glu Ile Tyr Gln Ser Val Lys Asn Gly Val Asn  
85 90 95

Gly Thr Leu Val Gly Asn Gly Leu Ser Gln Ala Glu Ala Thr Thr Leu  
100 105 110

Ser Lys Asn Phe Ser Asp Ile Lys Lys Glu Leu Asn Ala Lys Leu Gly  
115 120 125

Asn Phe Asn Asn Asn Asn Asn Asn Gly Leu Lys Asn Glu Pro Ile Tyr  
130 135 140

Ala Lys Val Asn Lys Lys Lys Ala Gly Gln Ala Ala Ser Leu Glu Glu  
145 150 155 160

Pro Ile Tyr Ala Gln Val Ala Lys Lys Val Asn Ala Lys Ile Asp Arg  
165 170 175

Leu Asn Gln Ile Ala Ser Gly Leu Gly Val Val Gly Gln Ala Ala Gly  
180 185 190

Phe Pro Leu Lys Arg His Asp Lys Val Asp Asp Leu Ser Lys Val Gly  
195 200 205

Leu Ser Arg Asn Gln Glu Leu Ala Gln Lys Ile Asp Asn Leu Asn Gln  
210 215 220

Ala Val Ser Glu  
225

<210> 26  
<211> 685  
<212> DNA  
<213> Helicobacter pylori

<400> 26  
aaaaatggca aaaataagga tttcagcaag gtaacgcaag caaaaagcga ccttgaaaat 60  
tccgttaaag atgtgatcat caatcaaaag gtaacggata aagttgataa tctcaatcaa 120  
gcggtatcag tggctaaagc aacgggtgat ttcagtaggg tagagcaagc gttagccgat 180  
ctcaaaaatt tctcaaagga gcaattggcc caacaagctc aaaaaaatga aagttctaat 240

CHIR0157 (updated 06-06-06).ST25.txt

gctagaaaaa aatctgaaat atatcaatcc gttagaatg gtgtgaatgg aaccctagtc	300
ggtaatgggt tatctcaagc agaagccaca actcttttcta aaaacttttc ggacatcaag	360
aaagagttga atgcaaaaact tggaaatttc aataacaata acaataatgg actcaaaaac	420
gaacccattt atgctaaagt taataaaaag aaagcagggc aagcagctag ccttgaagaa	480
cccatttacg ctcaagttgc taaaaaggta aatgcaaaaa ttgaccgact caatcaaata	540
gcaagtgggt tgggtgttgt agggcaagca gcgggcttcc ctttgaaaag gcatgataaa	600
gttgatgatc tcagtaaggt agggctttca aggaatcaag aattggctca gaaaattgac	660
aatctcaatc aagcggatc agaag	685

<210> 27  
 <211> 699  
 <212> DNA  
 <213> Helicobacter pylori

<400> 27	
gaattcaaaa atggcaaaaa taaggatttc agcaaggtaa cgcaagcaaa aagcgacctt	60
gaaaattccg ttaaagatgt gatcatcaat caaaaggtaa cggataaagt tgataatctc	120
aatcaagcgg tatcagtggc taaagcaacg ggtgatttca gtagggtaga gcaagcgtta	180
gccgatctca aaaatttctc aaaggagcaa ttggcccaac aagctcaaaa aaatgaaagt	240
ctcaatgcta gaaaaaaatc tgaaatatat caatccgtta agaatgggtg gaatggaacc	300
ctagtcggta atgggttatc tcaagcagaa gccacaactc tttctaaaaa cttttcggac	360
atcaagaaag agttgaatgc aaaacttgga aatttcaata acaataacaa taatggactc	420
aaaaacgaac ccatttatgc taaagttaat aaaaagaaag cagggaagc agctagcctt	480
gaagaaccca ttacgctca agttgctaaa aaggtaaagt caaaaattga ccgactcaat	540
caaatagcaa gtggtttggg tgttgtaggg caagcagcgg gcttcccttt gaaaaggcat	600
gataaagttg atgatctcag taaggtaggg ctttcaagga atcaagaatt ggctcagaaa	660
attgacaatc tcaatcaagc ggtatcagaa gccgaattc	699

<210> 28  
 <211> 15  
 <212> PRT  
 <213> Helicobacter pylori

<400> 28

Phe	Pro	Leu	Lys	Arg	His	Asp	Lys	Val	Asp	Asp	Leu	Ser	Lys	Val
1				5					10					15

<210> 29  
 <211> 6  
 <212> PRT  
 <213> Helicobacter pylori

<400> 29

Asn	Glu	Pro	Ile	Tyr	Ala
1				5	

CHIR0157 (updated 06-06-06).ST25.txt

<210> 30  
<211> 6  
<212> PRT  
<213> Helicobacter pylori

<400> 30

Glu Glu Pro Ile Tyr Ala  
1 5